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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=6; day=17; hr=11; min=7; sec=24; ms=56;]

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Reviewer Comments:

<110> APPLICANT: Novartis AG

<120> TITLE OF INVENTION: Organic Compound

<130> FILE REFERENCE: 4-32761P1/UNZ

<140> CURRENT APPLICATION NUMBER:10538201

<141> CURRENT FILING DATE:2006-03-08

<160> NUMBER OF SEQ ID NOS: 48

<170> SOFTWARE: PatentIn version 3.1

Please remove all subject line headers from the entire sequence listing. Example: "<110> APPLICANT: Novartis AG." should be "<110> Novartis AG.". This type of errors are seen globally throughout the sequences in teh sequence listing. Please make all necessary changes.

<210> SEQ ID NO 46

<211> LENGTH: 239

<212> TYPE: PRT

<213> ORGANISM: Pan paniscus

<400> SEQUENCE: 46

Gly	Lys	Val	Thr	Glu	Glu	Val	Val	Ala	Asn	Met	Pro	Glu	Gly	Leu	Thr
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Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Val	Thr
	20					25					30				
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Met	Asp	Leu	Val	Gln	Thr	Ser
	35				40				45						
Glu	Val	Met	Gln	Glu	Ser	Leu	Tyr	Pro	Ala	Ala	Gln	Leu	Cys	Pro	Ser
	50					55					60				
Phe	Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val
65					70					75					80

Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val	Pro	Ser	Ala	Gly	Ala	Ser	Ala		
				85					90					95			
Val	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Asn	Tyr	Glu		
			100					105					110				
Ser	Ile	Ile	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met		
		115					120					125					
Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly	Ile	Lys	Glu	Glu	Ile	Lys	Glu		
	130					135					140						
Pro	Glu	Ser	Ile	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile		
145				150					155					160			
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Ala	Glu	Pro		
			165					170					175				
Thr	Pro	Asp	Phe	Ser	Asp	Tyr	Ser	Glu	Met	Ala	Lys	Val	Glu	Gln	Pro		
		180						185					190				
Val	Pro	Asp	His	Ser	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu		
	195						200					205					
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Asp	Val	Pro	Gln	Lys		
	210					215					220						
Gln	Asp	Glu	Ala	Val	Met	Leu	Val	Lys	Glu	Asn	Leu	Pro	Glu	Thr			
225					230					235							

Miss-aligned Amino Acid numbering at position 18 onwards, Please correct the error.

Application No: 10538201 Version No: 2.0

Input Set:**Output Set:**

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Finished: 2010-06-09 19:47:49.232
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 566 ms
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Total Errors: 13
No. of SeqIDs Defined: 48
Actual SeqID Count: 48

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W 213	Artificial or Unknown found in <213> in SEQ ID (37)
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W 213	Artificial or Unknown found in <213> in SEQ ID (42)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (18)
E 323	Invalid/missing amino acid numbering SEQID (46)at Protein (20)
E 323	Invalid/missing amino acid numbering SEQID (46) POS (23)
E 323	Invalid/missing amino acid numbering SEQID (46)at Protein (25)

Input Set:

Output Set:

Started: 2010-06-09 19:47:41.666
Finished: 2010-06-09 19:47:49.232
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Error code	Error Description
E 323	Invalid/missing amino acid numbering SEQID (46) POS (28)
E 323	Invalid/missing amino acid numbering SEQID (46)at Protein (30)
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E 323	Invalid/missing amino acid numbering SEQID (46)at Protein (35)
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E 323	Invalid/missing amino acid numbering SEQID (46) POS (43)
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SEQUENCE LISTING

<110> APPLICANT: Novartis AG
<120> TITLE OF INVENTION: Organic Compound
<130> FILE REFERENCE: 4-32761P1/UNZ

<140> CURRENT APPLICATION NUMBER:10538201
<141> CURRENT FILING DATE:2006-03-08
<160> NUMBER OF SEQ ID NOS: 48
<170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (1)..(18)
<223> OTHER INFORMATION: rat NogoA_623-640
<400> SEQUENCE: 1

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1 5 10 15
Glu Ala

<210> SEQ ID NO 2
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: Mus musculus
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)..(221)
<223> OTHER INFORMATION: Variable part of Heavy Chain of 11C7 with leader sequence
<400> SEQUENCE: 2

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Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
20 25 30
Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45
Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80
Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95
Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110
Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125
Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
130 135 140
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175
Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val

	180		185		190										
Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Pro	Ser
	195				200								205		
Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala			
	210				215							220			

<210> SEQ ID NO 3
 <211> LENGTH: 238
 <212> TYPE: PRT
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CHAIN
 <222> LOCATION: (1)..(238)
 <223> OTHER INFORMATION: Light Chain of 11C7 with leader sequence
 <400> SEQUENCE: 3

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			20					25					30		
Thr	Ile	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Leu
		35					40					45			
Leu	His	Ser	Asp	Gly	Lys	Thr	Tyr	Leu	Asn	Trp	Leu	Leu	Gln	Arg	Pro
	50					55				60					
Gly	Gln	Ser	Pro	Lys	Arg	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Asp	Ser
65				70					75					80	
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
			85					90					95		
Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Tyr	Cys
			100					105					110		
Trp	Gln	Gly	Thr	His	Phe	Pro	Gln	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu
	115						120					125			
Glu	Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro
	130					135					140				
Ser	Ser	Glu	Gln	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu
145				150					155					160	
Asn	Asn	Phe	Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly
			165					170					175		
Ser	Glu	Arg	Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser
		180						185					190		
Lys	Asp	Ser	Thr	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp
	195					200						205			
Glu	Tyr	Glu	Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr
	210					215					220				
Ser	Thr	Ser	Pro	Ile	Val	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
225				230							235				

<210> SEQ ID NO 4
 <211> LENGTH: 3919
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (1)..(3579)
 <223> OTHER INFORMATION: Human NogoA
 <400> SEQUENCE: 4

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Met	Glu	Asp	Leu	Asp	Gln	Ser	Pro	Leu	Val	Ser	Ser	Ser	Asp	Ser	Pro	
1				5				10					15			
ccc	cgg	ccg	cag	ccc	gcg	ttc	aag	tac	cag	ttc	gtg	agg	gag	ccc	gag	96
Pro	Arg	Pro	Gln	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Arg	Glu	Pro	Glu	
			20					25					30			
gac	gag	gag	gaa	gaa	gag	gag	gag	gaa	gag	gag	gac	gag	gac	gaa	gac	144
Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Asp	
			35					40					45			
ctg	gag	gag	ctg	gag	gtg	ctg	gag	agg	aag	ccc	gcc	gcc	ggg	ctg	tcc	192
Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser	
			50				55						60			
gcg	gcc	cca	gtg	ccc	acc	gcc	cct	gcc	gcc	ggc	gcg	ccc	ctg	atg	gac	240
Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp	
65					70					75				80		
ttc	gga	aat	gac	ttc	gtg	ccg	ccg	gcg	ccc	cgg	gga	ccc	ctg	ccg	gcc	288
Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala	
				85					90					95		
gct	ccc	ccc	gtc	gcc	ccg	gag	cgg	cag	ccg	tct	tgg	gac	ccg	agc	ccg	336
Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro	
			100					105					110			
gtg	tcg	tcg	acc	gtg	ccc	gcg	cca	tcc	ccg	ctg	tct	gct	gcc	gca	gtc	384
Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val	
			115					120					125			
tcg	ccc	tcc	aag	ctc	cct	gag	gac	gac	gag	cct	ccg	gcc	cgg	cct	ccc	432
Ser	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	
			130				135					140				
cct	cct	ccc	ccg	gcc	agc	gtg	agc	ccc	cag	gca	gag	ccc	gtg	tgg	acc	480
Pro	Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr	
145					150				155					160		
ccg	cca	gcc	ccg	gct	ccc	gcc	gcg	ccc	ccc	tcc	acc	ccg	gcc	gcg	ccc	528
Pro	Pro	Ala	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ser	Thr	Pro	Ala	Ala	Pro	
				165					170				175			
aag	cgc	agg	ggc	tcc	tcg	ggc	tca	gtg	gat	gag	acc	ctt	ttt	gct	ctt	576
Lys	Arg	Arg	Gly	Ser	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	Phe	Ala	Leu	
			180					185					190			
cct	gct	gca	tct	gag	cct	gtg	ata	cgc	tcc	tct	gca	gaa	aat	atg	gac	624
Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Arg	Ser	Ser	Ala	Glu	Asn	Met	Asp	
			195				200					205				
ttg	aag	gag	cag	cca	ggg	aac	act	att	tcg	gct	ggg	caa	gag	gat	ttc	672
Leu	Lys	Glu	Gln	Pro	Gly	Asn	Thr	Ile	Ser	Ala	Gly	Gln	Glu	Asp	Phe	
			210				215					220				
cca	tct	gtc	ctg	ctt	gaa	act	gct	gct	tct	ctt	cct	tct	ctg	tct	cct	720
Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	Ser	Leu	Ser	Pro	
225					230				235				240			
ctc	tca	gcc	gct	tct	ttc	aaa	gaa	cat	gaa	tac	ctt	ggg	aat	ttg	tca	768
Leu	Ser	Ala	Ala	Ser	Phe	Lys	Glu	His	Glu	Tyr	Leu	Gly	Asn	Leu	Ser	
				245					250				255			
aca	gta	tta	ccc	act	gaa	gga	aca	ctt	caa	gaa	aat	gtc	agt	gaa	gct	816
Thr	Val	Leu	Pro	Thr	Glu	Gly	Thr	Leu	Gln	Glu	Asn	Val	Ser	Glu	Ala	
			260					265				270				
tct	aaa	gag	gtc	tca	gag	aag	gca	aaa	act	cta	ctc	ata	gat	aga	gat	864
Ser	Lys	Glu	Val	Ser	Glu	Lys	Ala	Lys	Thr	Leu	Leu	Ile	Asp	Arg	Asp	
			275				280					285				
tta	aca	gag	ttt	tca	gaa	tta	gaa	tac	tca	gaa	atg	gga	tca	tcg	ttc	912
Leu	Thr	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	Gly	Ser	Ser	Phe	
			290				295					300				
agt	gtc	tct	cca	aaa	gca	gaa	tct	gcc	gta	ata	gta	gca	aat	cct	agg	960

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg	
305 310 315 320	
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt	1008
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser	
325 330 335	
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa	1056
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys	
340 345 350	
ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt	1104
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser	
355 360 365	
ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat	1152
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr	
370 375 380	
gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag	1200
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys	
385 390 395 400	
gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg	1248
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu	
405 410 415	
gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act	1296
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr	
420 425 430	
aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc	1344
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro	
435 440 445	
agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt	1392
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys	
450 455 460	
gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt	1440
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe	
465 470 475 480	
cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa	1488
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys	
485 490 495	
ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc	1536
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr	
500 505 510	
aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat	1584
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp	
515 520 525	
tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca	1632
Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala	
530 535 540	
aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa	1680
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu	
545 550 555 560	
agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa	1728
Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys	
565 570 575	
atg gac ttg gtt caa aca tca gaa gtt atg caa gag tca ctc tat cct	1776
Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro	
580 585 590	
gca gca cag ctt tgc cca tca ttt gaa gag tca gaa gct act cct tca	1824
Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser	
595 600 605	
cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt	1872

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val	
610 615 620	
cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa	1920
Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu	
625 630 635 640	
gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc	1968
Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro	
645 650 655	
cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga	2016
Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly	
660 665 670	
ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa	2064
Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln	
675 680 685	
gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa	2112
Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu	
690 695 700	
aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa	2160
Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu	
705 710 715 720	
atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa	2208
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu	
725 730 735	
gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca	2256
Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser	
740 745 750	
ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa	2304
Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys	
755 760 765	
gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat	2352
Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn	
770 775 780	
aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg	2400
Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu	
785 790 795 800	
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct	2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro	
805 810 815	
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg	2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met	
820 825 830	
gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct	2544
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser	
835 840 845	
aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca	2592
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro	
850 855 860	
att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat	2640
Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp	
865 870 875 880	
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac	2688
Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His	
885 890 895	
aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc	2736
Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys	
900 905 910	
aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt	2784

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val

915

920

925

gaa gag aaa